RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: *10/510,627*
Source: *PCT/IP*
Date Processed by STIC: *10/16/04*

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.2 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
     http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
   U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

PCT

RAW SEQUENCE LISTING   DATE: 10/16/2004
PATENT APPLICATION: US/10/510,627   TIME: 08:51:44

Input Set : **N:\FATIMA\10510627.txt**
Output Set: **N:\CRF4\10162004\J510627.raw**

```
 3 <110> APPLICANT: TOKAI UNIVERSITY
 4        KYOWA HAKKO KOGYO CO., LTD.
 5        KYOWA MEDEX CO., LTD.
 7 <120> TITLE OF INVENTION: A diagnostic method and a diagnostic agent for
 8        leukemia, preleukemia and leukemic malignant hemopathy
10 <130> FILE REFERENCE: 11470WO1
```
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/510,627
C--> 13 <141> CURRENT FILING DATE: 2004-10-08
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15 <150> PRIOR APPLICATION NUMBER: JP P2002-106786
16 <151> PRIOR FILING DATE: 2002-04-09
18 <160> NUMBER OF SEQ ID NOS: 11
20 <170> SOFTWARE: PatentIn Ver. 2.1
```

pp 1-3

Does Not Comply
Corrected Diskette Needed

ERRORED SEQUENCES

```
270 <210> SEQ ID NO: 11
271 <211> LENGTH: 18
272 <212> TYPE: DNA
273 <213> ORGANISM: Artificial Sequence
```
W--> 275 (220) FEATURE:
W--> 275 (223) OTHER INFORMATION:
W--> 275 <400> 11
```
276 ttttgggggc tttggtgg                                    18
```
E--> 288 (8/8) delete

RAW SEQUENCE.LISTING ERROR SUMMARY   DATE: 10/16/2004
PATENT APPLICATION: US/10/510,627   TIME: 08:51:45

Input Set : **N:\FATIMA\10510627.txt**
Output Set: **N:\CRF4\10162004\J510627.raw**

erro explanation

Use of <220> Feature(NEW RULES):
Sequence(s)__are missing the <220> Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence"
or"Unknown". Please explain source of genetic material in <220> to <223>
section (See "Federal Register," 6/01/98, Vol. 63, No. 104,pp.29631-32)
(Sec.1.823 of new Rules)

Seq#:8,9,10,11. *each of these sequences has the above error*

see p.3 for more errors

Ala Leu Gly Leu Pro Ala Gly Arg Gly Asp Glu Asn Pro Ala Gly Thr
          35   40   45

(1 / 8)

T do *not* show page
numbers in the computer
readable file of the
Sequence Listing

please
remove
all page
numbers
in submitted
Sequence Listing
file

(per 1.824 of Sequence Rules)

Input Set : **N:\FATIMA\10510627.txt**
Output Set: **N:\CRF4\10162004\J510627.raw**

L:12 M:270 C: Current Application Number differs, Replaced Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:228 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
L:247 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:8, <213>
ORGANISM:Artificial Sequence
L:247 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:8, <213>
ORGANISM:Artificial Sequence
L:247 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:8,Line#:247
L:252 M:259 W: Allowed number of lines exceeded, <210> SEQ ID NO
L:257 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:9, <213>
ORGANISM:Artificial Sequence
L:257 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:9, <213>
ORGANISM:Artificial Sequence
L:257 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:257
L:266 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:10, <213>
ORGANISM:Artificial Sequence
L:266 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:10, <213>
ORGANISM:Artificial Sequence
L:266 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:10,Line#:266
L:275 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:11, <213>
ORGANISM:Artificial Sequence
L:275 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:11, <213>
ORGANISM:Artificial Sequence
L:275 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:11,Line#:275
L:288 M:254 E: No. of Bases conflict, LENGTH:Input:8 Counted:19 SEQ:11
L:288 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:288 M:252 E: No. of Seq. differs, <211> LENGTH:Input:18 Found:19 SEQ:11